

5' ATG GGA ATG GCC TGC CTT ACG ATG ACA GAA ATG GAG GGA ACA TCC ACC TCT TCT
 Met Gly Met Ala Cys Leu Thr Met Thr Glu Met Glu Gly Thr Ser Thr Ser Ser

348 357 366 375 384 393
 402 411 420 429 438 447
 ATA TAT CAG AAT GGT GAT ATT TCT GGA AAT GCC AAT TCT ATG AAG CAA ATA GAT
 Ile Tyr Gln Asn Gly Asp Ile Ser Gly Asn Ala Asn Ser Met Lys Gln Ile Asp

456 465 474 483 492 501
 CCA GTT CTT CAG GTG TAT CTT TAC CAT TCC CTT GGG AAA TCT GAG GCA GAT TAT
 Pro Val Leu Gln Val Tyr Leu Tyr His Ser Leu Gly Lys Ser Glu Ala Asp Tyr

510 519 528 537 546 555
 CTG ACC TTT CCA TCT GGG GAG TAT GTT GGA GAA GAA ATC TGT ATT GCT GCT TCT
 Leu Thr Phe Pro Ser Gly Glu Tyr Val Gly Glu Glu Ile Cys Ile Ala Ala Ser

564 573 582 591 600 609
 AAA GCT TGT GGT ATC ACA CCT GTG TAT CAT AAT ATG TTT GCT TTA ATG AGT GAA
 Lys Ala Cys Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu Met Ser Glu

618 627 636 645 654 663
 ACA GAA AGG ATC TGG TAT CCA CCC AAC CAT GTC TTC CAT ATA GAT GAG TCA ACC
 Thr Glu Arg Ile Trp Tyr Pro Pro Asn His Val Phe His Ile Asp Glu Ser Thr

672 681 690 699 708 717
 AGG CAT AAT GTA CTC TAC AGA ATA AGA TTT TAC TTT CCT CGT TGG TAT TGC AGT
 Arg His Asn Val Leu Tyr Arg Ile Arg Phe Tyr Phe Pro Arg Trp Tyr Cys Ser

726 735 744 753 762 771
 GGC AGC AAC AGA GCC TAT CGG CAT GGA ATA TCT CGA GGT GCT GAA GCT CCT CTT
 Gly Ser Asn Arg Ala Tyr Arg His Gly Ile Ser Arg Gly Ala Glu Ala Pro Leu

780 789 798 807 816 825
 CTT GAT GAC TTT GTC ATG TCT TAC CTC TTT GCT CAG TCG CGG CAT GAT TTT GTG
 Leu Asp Asp Phe Val Met Ser Tyr Leu Phe Ala Gln Trp Arg His Asp Phe Val

834 843 852 861 870 879
 CAT GGA TGG ATA AAA GTA CCT GTG ACT CAT GAA ACA CAG GAA GAA TGT CTT GGG
 His Gly Trp Ile Lys Val Pro Val Thr His Glu Thr Gln Glu Glu Cys Leu Gly

888 897 906 915 924 933
 ATG ACA GTG TTA GAT ATG ATG AGA ATA GCC AAA GAA AAC GAT CAA ACC CCA CTG
 Met Thr Val Leu Asp Met Met Arg Ile Ala Lys Glu Asn Asp Gln Thr Pro Leu

942 951 960 969 978 987
 GCC ATC TAT AAC TCT ATC AGC TAC AAG ACA TTC TTA CCA CAA TGT ATT CGA GCA
 Ala Ile Tyr Asn Ser Ile Ser Tyr Lys Thr Phe Leu Pro Gln Cys Ile Arg Ala

FIGURE 1A

996	1005	1014	1023	1032	1041
AAG ATC CAA GAC TAT CAT ATT TTG ACA AGG AAG CGA ATA AGG TAC AGA TTT CGC					
Lys Ile Gln Asp Tyr His Ile Leu Thr Arg Lys Arg Ile Arg Tyr Arg Phe Arg					
1050	1059	1068	1077	1086	1095
AGA TTT ATT CAG CAA TTC AGC CAA TGC AAA GCC ACT GCC AGA AAC TTG AAA CTT					
Arg Phe Ile Gln Gln Phe Ser Gln Cys Lys Ala Thr Ala Arg Asn Leu Lys Leu					
1104	1113	1122	1131	1140	1149
AAG TAT CTT ATA AAT CTG GAA ACT CTG CAG TCT GCC TTC TAC ACA GAG AAA TTT					
Lys Tyr Leu Ile Asn Leu Glu Thr Leu Gln Ser Ala Phe Tyr Thr Glu Lys Phe					
1158	1167	1176	1185	1194	1203
GAA GTA AAA GAA CCT GGA AGT GGT CCT TCA GGT GAG GAG ATT TTT GCA ACC ATT					
Glu Val Lys Glu Pro Gly Ser Gly Pro Ser Gly Glu Glu Ile Phe Ala Thr Ile					
1212	1221	1230	1239	1248	1257
ATA ATA ACT GGA AAC GGT GGA ATT CAG TGG TCA AGA GGG AAA CAT AAA GAA AGT					
Ile Ile Thr Gly Asn Gly Gly Ile Gln Trp Ser Arg Gly Lys His Lys Glu Ser					
1266	1275	1284	1293	1302	1311
GAG ACA CTG ACA GAA CAG GAT TTA CAG TTA TAT TGC GAT TTT CCT AAT ATT ATT					
Glu Thr Leu Thr Glu Gln Asp Leu Gln Leu Tyr Cys Asp Phe Pro Asn Ile Ile					
1320	1329	1338	1347	1356	1365
GAT GTC AGT ATT AAG CAA GCA AAC CAA GAG GGT TCA AAT GAA AGC CGA GTT GTA					
Asp Val Ser Ile Lys Gln Ala Asn Gln Glu Gly Ser Asn Glu Ser Arg Val Val					
1374	1383	1392	1401	1410	1419
ACT ATC CAT AAG CAA GAT GGT AAA AAT CTG GAA ATT GAA CTT AGC TCA TTA AGG					
Thr Ile His Lys Gln Asp Gly Lys Asn Leu Glu Ile Glu Leu Ser Ser Leu Arg					
1428	1437	1446	1455	1464	1473
GAA GCT TTG TCT TTC GTG TCA TTA ATT GAT GGA TAT TAT AGA TTA ACT GCA GAT					
Glu Ala Leu Ser Phe Val Ser Leu Ile Asp Gly Tyr Tyr Arg Leu Thr Ala Asp					
1482	1491	1500	1509	1518	1527
GCA CAT CAT TAC CTC TGT AAA GAA GTA GCA CCT CCA GCC GTG CTT GAA AAT ATA					
Ala His His Tyr Leu Cys Lys Glu Val Ala Pro Pro Ala Val Leu Glu Asn Ile					
1536	1545	1554	1563	1572	1581
CAA AGC AAC TGT CAT GGC CCA ATT TCG ATG GAT TTT GCC ATT AGT AAA CTG AAG					
Gln Ser Asn Cys His Gly Pro Ile Ser Met Asp Phe Ala Ile Ser Lys Leu Lys					
1590	1599	1608	1617	1626	1635
AAA GCA GGT AAT CAG ACT GGA CTG TAT GTA CTT CGA TGC AGT CCT AAG GAC TTT					
Lys Ala Gly Asn Gln Thr Gly Leu Tyr Val Leu Arg Cys Ser Pro Lys Asp Phe					

FIGURE 1B

1644 1653 1662 1671 1680 1689
 AAT AAA TAT TTT TTG ACT TTT GCT GTC GAG CGA GAA AAT GTC ATT GAA TAT AAA
 Asn Lys Tyr Phe Leu Thr Phe Ala Val Glu Arg Glu Asn Val Ile Glu Tyr Lys

1698 1707 1716 1725 1734 1743
 CAC TGT TTG ATT ACA AAA AAT GAG AAT GAA GAG TAC AAC CTC AGT GGG ACA AAG
 His Cys Leu Ile Thr Lys Asn Glu Asn Glu Glu Tyr Asn Leu Ser Gly Thr Lys

1752 1761 1770 1779 1788 1797
 AAG AAC TTC AGC AGT CTT AAA GAT CTT TTG AAT TGT TAC CAG ATG GAA ACT GTT
 Lys Asn Phe Ser Ser Leu Lys Asp Leu Leu Asn Cys Tyr Gln Met Glu Thr Val

1806 1815 1824 1833 1842 1851
 CGC TCA GAC AAT ATA ATT TTC CAG TTT ACT AAA TGC TGT CCC CCA AAG CCA AAA
 Arg Ser Asp Asn Ile Ile Phe Gln Phe Thr Lys Cys Cys Pro Pro Lys Pro Lys

1860 1869 1878 1887 1896 1905
 GAT AAA TCA AAC CTT CTA GTC TTC AGA ACG AAT GGT GTT TCT GAT GTA CCA ACC
 Asp Lys Ser Asn Leu Leu Val Phe Arg Thr Asn Gly Val Ser Asp Val Pro Thr

1914 1923 1932 1941 1950 1959
 TCA CCA ACA TTA CAG AGG CCT ACT CAT ATG AAC CAA ATG GTG TTT CAC AAA ATC
 Ser Pro Thr Leu Gln Arg Pro Thr His Met Asn Gln Met Val Phe His Lys Ile

1968 1977 1986 1995 2004 2013
 AGA AAT GAA GAT TTG ATA TTT AAT GAA AGC CTT GGC CAA GGC ACT TTT ACA AAG
 Arg Asn Glu Asp Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe Thr Lys

2022 2031 2040 2049 2058 2067
 ATT TTT AAA GGC GTA CGA AGA GAA GTA GGA GAC TAC GGT CAA CTG CAT GAA ACA
 Ile Phe Lys Gly Val Arg Arg Glu Val Gly Asp Tyr Gly Gln Leu His Glu Thr

2076 2085 2094 2103 2112 2121
 GAA GTT CTT TTA AAA GTT CTG GAT AAA GCA CAC AGG AAC TAT TCA GAG TCT TTC
 Glu Val Leu Leu Lys Val Leu Asp Lys Ala His Arg Asn Tyr Ser Glu Ser Phe

2130 2139 2148 2157 2166 2175
 TTT GAA GCA GCA AGT ATG ATG AGC AAG CTT TCT CAC AAG CAT TTG GTT TTA AAT
 Phe Glu Ala Ala Ser Met Met Ser Lys Leu Ser His Lys His Leu Val Leu Asn

2184 2193 2202 2211 2220 2229
 TAT GGA GTA TGT GTC TGT GGA GAC GAG AAT ATT CTG GTT CAG GAG TTT GTA AAA
 Tyr Gly Val Cys Val Cys Gly Asp Glu Asn Ile Leu Val Gln Glu Phe Val Lys

2238 2247 2256 2265 2274 2283
 TTT GGA TCA CTA GAT ACA TAT CTG AAA AAG AAT AAA AAT TGT ATA AAT ATA TTA
 Phe Gly Ser Leu Asp Thr Tyr Leu Lys Lys Asn Lys Asn Cys Ile Asn Ile Leu

FIGURE 1C

2292	2301	2310	2319	2323	2337
TGG AAA CTT GAA GTT GCT	AAA CAG TTG	GCA TGG GCC	ATG CAT TTT	CTA GAA GAA	
Trp Lys Leu Glu Val Ala	Lys Gln Leu	Ala Trp Ala	Met His Phe	Leu Glu Glu	
2346	2355	2364	2373	2382	2391
AAC ACC CTT ATT CAT GGG	AAT GTA TGT	GCC AAA AAT	ATT CTG CTT	ATC AGA GAA	
Asn Thr Leu Ile His Gly	Asn Val Cys	Ala Lys Asn	Ile Leu Leu	Ile Arg Glu	
2400	2409	2418	2427	2436	2445
GAA GAC AGG AAG ACA GGA	AAT CCT CCT	TTC ATC AAA	CTT AGT GAT	CCT GGC ATT	
Glu Asp Arg Lys Thr Gly	Asn Pro Pro	Phe Ile Lys	Leu Ser Asp	Pro Gly Ile	
2454	2463	2472	2481	2490	2499
AGT ATT ACA GTT TTG CCA	AAG GAC ATT	CTT CAG GAG	AGA ATA CCA	TGG GTA CCA	
Ser Ile Thr Val Leu Pro	Lys Asp Ile	Leu Gln Glu	Arg Ile Pro	Trp Val Pro	
2508	2517	2526	2535	2544	2553
CCT GAA TGC ATT GAA AAT	CCT AAA AAT	TTA AAT TTG	GCA ACA GAC	AAA TGG AGT	
Pro Glu Cys Ile Glu Asn	Pro Lys Asn	Leu Asn Leu	Ala Thr Asp	Lys Trp Ser	
2562	2571	2580	2589	2593	2607
TTT GGT ACC ACT TTG TGG	GAA ATC TGC	AGT GGA GGA	GAT AAA CCT	CTA AGT GCT	
Phe Gly Thr Thr Leu Trp	Glu Ile Cys	Ser Gly Gly	Asp Lys Pro	Leu Ser Ala	
2616	2625	2634	2643	2652	2661
CTG GAT TCT CAA AGA AAG	CTA CAA TTT	TAT GAA GAT	AGG CAT CAG	CTT CCT GCA	
Leu Asp Ser Gln Arg Lys	Leu Gln Phe	Tyr Glu Asp	Arg His Gln	Leu Pro Ala	
2670	2679	2688	2697	2706	2715
CCA AAG TGG GCA GAA TTA	GCA AAC CTT	ATA AAT AAT	TGT ATG GAT	TAT GAA CCA	
Pro Lys Trp Ala Glu Leu	Ala Asn Leu	Ile Asn Asn	Cys Met Asp	Tyr Glu Pro	
2724	2733	2742	2751	2760	2769
GAT TTC AGG CCT TCT TTC	AGA GCC ATC	ATA CGA GAT	CTT AAC AGT	TTG TTT ACT	
Asp Phe Arg Pro Ser Phe	Arg Ala Ile	Ile Arg Asp	Leu Asn Ser	Leu Phe Thr	
2778	2787	2796	2805	2814	2823
CCA GAT TAT GAA CTA TTA	ACA GAA AAT	GAC ATG TTA	CCA AAT ATG	AGG ATA GGT	
Pro Asp Tyr Glu Leu Leu	Thr Glu Asn	Asp Met Leu	Pro Asn Met	Arg Ile Gly	
2832	2841	2850	2859	2868	2877
GCC TTG GGG TTT TCT GGT	GCC TTT GAA	GAC CGG GAT	CCT ACA CAG	TTT GAA GAG	
Ala Leu Gly Phe Ser Gly	Ala Phe Glu	Asp Arg Asp	Pro Thr Gln	Phe Glu Glu	
2886	2895	2904	2913	2922	2931

FIGURE 1D

AGA CAT TTG AAA TTT CTA CAG CAA CTT GGC AAG GGT AAT TTT GGG AGT GTG GAG
Arg His Leu Lys Phe Leu Gln Gln Leu Gly Lys Gly Asn Phe Gly Ser Val Glu

2940 2949 2958 2967 2976 2985
ATG TGC CGG TAT GAC CCT CTA CAG GAC AAC ACT GGG GAG GTG GTC GCT GTA AAA
Met Cys Arg Tyr Asp Pro Leu Gln Asp Asn Thr Gly Glu Val Val Ala Val Lys

2994 3003 3012 3021 3030 3039
AAG CTT CAG CAT AGT ACT GAA GAG CAC CTA AGA GAC TTT GAA AGG GAA ATT GAA
Lys Leu Gln His Ser Thr Glu Glu His Leu Arg Asp Phe Glu Arg Glu Ile Glu

3048 3057 3066 3075 3084 3093
ATC CTG AAA TCC CTA CAG CAT GAC AAC ATT GTA AAG TAC AAG GGA GTG TGC TAC
Ile Leu Lys Ser Leu Gln His Asp Asn Ile Val Lys Tyr Lys Gly Val Cys Tyr

3102 3111 3120 3129 3138 3147
AGT GCT GGT CGG CGT AAT CTA AAA TTA ATT ATG GAA TAT TTA CCA TAT GGA AGT
Ser Ala Gly Arg Arg Asn Leu Lys Leu Ile Met Glu Tyr Leu Pro Tyr Gly Ser

3156 3165 3174 3183 3192 3201
TTA CGA GAC TAT CTT CAA AAA CAT AAA GAA CGG ATA GAT CAC ATA AAA CTT CTG
Leu Arg Asp Tyr Leu Gln Lys His Lys Glu Arg Ile Asp His Ile Lys Leu Leu

3210 3219 3228 3237 3246 3255
CAG TAC ACA TCT CAG ATA TGC AAG GGT ATG GAG TAT CTT GGT ACA AAA AGG TAT
Gln Tyr Thr Ser Gln Ile Cys Lys Gly Met Glu Tyr Leu Gly Thr Lys Arg Tyr

3264 3273 3282 3291 3300 3309
ATC CAC AGG GAT CTG GCA ACG AGA AAT ATA TTG GTG GAG AAC GAG AAC AGA GTT
Ile His Arg Asp Leu Ala Thr Arg Asn Ile Leu Val Glu Asn Glu Asn Arg Val

3318 3327 3336 3345 3354 3363
AAA ATT GGR GAT TTT GGG TTA ACC AAA GTC TTG CCA CAA GAC AAA GAA TAC TAT
Lys Ile Gly Asp Phe Gly Leu Thr Lys Val Leu Pro Gln Asp Lys Glu Tyr Tyr

3372 3381 3390 3399 3408 3417
AAA GTA AAA GAA CCT GGT GAA AGT CCC ATA TTC TGG TAT GCT CCA GAA TCA CTG
Lys Val Lys Glu Pro Gly Glu Ser Pro Ile Phe Trp Tyr Ala Pro Glu Ser Leu

3426 3435 3444 3453 3462 3471
ACA GAG AGC AAG TTT TCT GTG GCC TCA GAT GTT TGG ACC TTT GGA GTG GTT CTG
Thr Glu Ser Lys Phe Ser Val Ala Ser Asp Val Trp Ser Phe Gly Val Val Leu

3480 3489 3498 3507 3516 3525
TAT GAA CTT TTC ACA TAC ATT GAG AAG AGT AAA AGT CCA CCA GCG GAA TTT ATG
Tyr Glu Leu Phe Thr Tyr Ile Glu Lys Ser Lys Ser Pro Pro Ala Glu Phe Met

3534 3543 3552 3561 3570 3579
CGT ATG ATT GGC AAT GAC AAA CAA GGA CAG ATG ATC GTG TTC CAT TTG ATA GAA
Arg Met Ile Gly Asn Asp Lys Gln Gly Gln Met Ile Val Phe His Leu Ile Glu

FIGURE 1E

3588	3597	3606	3615	3624	3633
CTT TTG AAG AAT AAT GGA AGA TTA CCA AGA CCA GAT GGA TGC CCA GAT GAG ATC					
Leu Leu Lys Asn Asn Gly Arg Leu Pro Arg Pro Asp Gly Cys Pro Asp Glu Ile					
3642	3651	3660	3669	3678	3687
TAT ATG ATC ATG ACA GAA TGC TGG AAC AAT AAT GTA AAT CAA CGC CCC TCC TTT					
Tyr Met Ile Met Thr Glu Cys Trp Asn Asn Asn Val Asn Gln Arg Pro Ser Phe					
3696	3705	3714	3723	3732	
AGG GAT CTA GCT CTT CGA GTG GAT CAA ATA AGG GAT AAC ATG GCT GGA TGA 3'					
Arg Asp Leu Ala Leu Arg Val Asp Gln Ile Arg Asp Asn Met Ala Gly ***					

FIGURE 1F

M G M A C L T M T E M E . T S T S . . . Q N G D I . G . A N
 M G M A C L T M T E M E G T S T S S V H Q N G D I S G S A N
 10 20 30
 1 M G M A C L T M T E M E A T S T S P V H Q N G D I P G S A N
 1 M G M A C L T M T E M E G T S T S S I Y Q N G D I S G N A N
 S . K Q I . P V L Q V Y L Y H S L G . . E . . Y L . F P S G
 S V K Q I D P V L Q V Y L Y H S L G Q A E G D Y L T F P S G
 40 50 60
 31 S V K Q I E P V L Q V Y L Y H S L G Q A E G E Y L K F P S G
 31 S M K Q I D P V L Q V Y L Y H S L G K S E A D Y L T F P S G
 E Y V . E E I C . A A S K A C G I T P V Y H N M F A L M S E
 E Y V G E E I C V A A S K A C G I T P V Y H N M F A L M S E
 70 80 90
 61 E Y V A E E I C V A A S K A C G I T P V Y H N M F A L M S E
 61 E Y V G E E I C I A A S K A C G I T P V Y H N M F A L M S E
 T E R I W Y P P N H V F H I D E S T R H . . L Y R I R F Y F
 T E R I W Y P P N H V F H I D E S T R H D V L Y R I R F Y F
 100 110 120
 91 T E R I W Y P P N H V F H I D E S T R H D I L Y R I R F Y F
 91 T E R I W Y P P N H V F H I D E S T R H N V L Y R I R F Y F
 P . W Y C S G S . R . Y R . G . S R G A E A P L L D D F V M
 P H W Y C S G S S R A Y R H G V S R G A E A P L L D D F V M
 130 140 150
 121 P H W Y C S G S S R T Y R Y G V S R G A E A P L L D D F V M
 121 P R W Y C S G S N R A Y R H G I S R G A E A P L L D D F V M
 S Y L F . Q W R H D F V H G W I K V P V T H E T Q E E C L G
 S Y L F A Q W R H D F V H G W I K V P V T H E T Q E E C L G
 160 170 180
 151 S Y L F V Q W R H D F V H G W I K V P V T H E T Q E E C L G
 151 S Y L F A Q W R H D F V H G W I K V P V T H E T Q E E C L G
 M . V L D M M R I A K E . D Q T P L A . Y N S . S Y K T F L
 M A V L D M M R I A K E N D Q T P L A V Y N S V S Y K T F L
 190 200 210
 181 M A V L D M M R I A K E K D Q T P L A V Y N S V S Y K T F L
 181 M T V L D M M R I A K E N D Q T P L A I Y N S I S Y K T F L

FIGURE 2A

P . C . R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F
 P Q C V R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F
 220 230 240
 211 **P K C V R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F**
 211 **P Q C I R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F**
 S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E . F
 S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E Q F
 250 260 270
 241 **S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E Q F**
 241 **S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E K F**
 E V K E . . . G P S G E E I F A T I I I T G N G G I Q W S R
 E V K E S G S G P S G E E I F A T I I I T G N G G I Q W S R
 280 290 300
 271 **E V K E S A R G P S G E E I F A T I I I T G N G G I Q W S R**
 271 **E V K E P G S G P S G E E I F A T I I I T G N G G I Q W S R**
 G K H K E S E T L T E Q D . Q L Y C D F P . I I D V S I K Q
 G K H K E S E T L T E Q D V Q L Y C D F P D I I D V S I K Q
 310 320 330
 301 **G K H K E S E T L T E Q D V Q L Y C D F P D I I D V S I K Q**
 301 **G K H K E S E T L T E Q D L Q L Y C D F P N I I D V S I K Q**
 A N Q E . S N E S R . V T . H K Q D G K . L E I E L S S L .
 A N Q E G S N E S R V V T V H K Q D G K V L E I E L S S L K
 340 350 360
 331 **A N Q E C S N E S R I V T V H K Q D G K V L E I E L S S L K**
 331 **A N Q E G S N E S R V V T I H K Q D G K N L E I E L S S L R**
 E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P
 E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P
 370 380 390
 361 **E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P**
 361 **E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P**

FIGURE 2B

A V L E N I . S N C H G P I S M D F A I S K L K K A G N Q T
 A V L E N I Q S N C H G P I S M D F A I S K L K K A G N Q T
 400 410 420
 391 **A V L E N I H S N C H G P I S M D F A I S K L K K A G N Q T**
 391 **A V L E N I Q S N C H G P I S M D F A I S K L K K A G N Q T**
 G L Y V L R C S P K D F N K Y F L T F A V E R E N V I E Y K
 G L Y V L R C S P K D F N K Y F L T F A V E R E N V I E Y K
 430 440 450
 421 **G L Y V L R C S P K D F N K Y F L T F A V E R E N V I E Y K**
 421 **G L Y V L R C S P K D F N K Y F L T F A V E R E N V I E Y K**
 H C L I T K N E N . E Y N L S G T . N F S . L K D L L N C
 H C L I T K N E N E G E Y N L S G T N K N F S S L K D L L N C
 460 470 480
 451 **H C L I T K N E N E G E Y N L S G T N R N F S N L R D L L N C**
 451 **H C L I T K N E N E G E Y N L S G T K K N F S S L R D L L N C**
 Y Q M E T V R S D . I I F Q F T K C C P P K P K D K S N L L
 Y Q M E T V R S D S I I F Q F T K C C P P K P K D K S N L L
 490 500 510
 481 **Y Q M E T V R S D S I I F Q F T K C C P P K P K D K S N L L**
 481 **Y Q M E T V R S D N I I F Q F T K C C P P K P K D K S N L L**
 V F R T N G . S D V . S P T L Q R . . . N Q M V F H K I
 V F R T N G V S D V Q I S P T L Q R H T N V N Q M V F H K I
 520 530 540
 511 **V F R T N G I S D V Q I S P T L Q R H N N V N Q M V F H K I**
 511 **V F R T N G V S D V P T S P T L Q R P T H M N Q M V F H K I**
 R N E D L I F N E S L G Q G T F T K I F K G V R R E V G D Y
 R N E D L I F N E S L G Q G T F T K I F K G V R R E V G D Y
 550 560 570
 541 **R N E D L I F N E S L G Q G T F T R I F K G V R R E V G D Y**
 541 **R N E D L I F N E S L G Q G T F T R I F K G V R R E V G D Y**
 G Q L H . T E V L L K V L D K A H R N Y S E S F F E A A S M
 G Q L H E T E V L L K V L D K A H R N Y S E S F F E A A S M
 580 590 600
 571 **G Q L H K T E V L L K V L D K A H R N Y S E S F F E A A S M**
 571 **G Q L H E T E V L L K V L D K A H R N Y S E S F F E A A S M**

FIGURE 2C

MS . LSHKHLVLNYGVCVCG . ENILVQEFVK
MSQLSHKHLVLNYGVCVCGDENILVQEFVK

610 620 630

601 MSQ LSHKHLVLNYGVCVCGE ENILVQEFVK
601 MSK LSHKHLVLNYGVCVCGD ENILVQEFVK

FGSLDTYLKKKNKN . INILWKL . VAKQLAWA
FGSLDTYLKKKNKNSINILWKLGVAKQLAWA

640 650 660

631 FGS LDTYLKKKNKNS INILWKLGVAKQLAWA
631 FGS LDTYLKKKNKNC INILWKLGVAKQLAWA

MHFLEE . LIHGNCVCAKNILLIREEDR . TG
MHFLEENSLIHGNCVCAKNILLIREEDRKTG

670 680 690

661 MHFLEE KSLIHGNCVCAKNILLIREEDRRTG
661 MHFLEEN TLIHGNCVCAKNILLIREEDRKTG

NPPFIKLSDPGISITVLPKDILOERIPWVP
NPPFIKLSDPGISITVLPKDILOERIPWVP

700 710 720

691 NPPFIKLSDPGISITVLPKDILOERIPWVP
691 NPPFIKLSDPGISITVLPKDILOERIPWVP

PECIENPKNLNLATDKWSFGTTLWEICSGG
PECIENPKNLNLATDKWSFGTTLWEICSGG

730 740 750

721 PECIENPKNLNLATDKWSFGTTLWEICSGG
721 PECIENPKNLNLATDKWSFGTTLWEICSGG

DKPLSALDSQRKLOFYED . HQLPAPKW . EL
DKPLSALDSQRKLOFYEDKHQLPAPKWAEL

760 770 780

751 DKPLSALDSQRKLOFYEDKHQLPAPKWTEL
751 DKPLSALDSQRKLOFYEDRHQLPAPKWAEL

ANLINNCMDYEPDFRP . FRA . IRDLNSLFT
ANLINNCMDYEPDFRPAPRAVIRDLNSLFT

790 800 810

781 ANLINNCMDYEPDFRPAFRAVIRDLNSLFT
781 ANLINNCMDYEPDFRPSFRAVIRDLNSLFT

FIGURE 2D

PDYELLTENDMLPNMRIGALGFSGAFEDRD
 PDYELLTENDMLPNMRIGALGFSGAFEDRD
 820 830 840
 811 PDYELLTENDMLPNMRIGALGFSGAFEDRD
 811 PDYELLTENDMLPNMRIGALGFSGAFEDRD
 PTQFEERHLKFLQQLGKGNFGSVEMCRYDP
 PTQFEERHLKFLQQLGKGNFGSVEMCRYDP
 850 860 870
 841 PTQFEERHLKFLQQLGKGNFGSVEMCRYDP
 841 PTQFEERHLKFLQQLGKGNFGSVEMCRYDP
 LQDNTGEVVAVKKLQHSSTEEHLRDFEREIE
 LQDNTGEVVAVKKLQHSSTEEHLRDFEREIE
 880 890 900
 871 LQDNTGEVVAVKKLQHSSTEEHLRDFEREIE
 871 LQDNTGEVVAVKKLQHSSTEEHLRDFEREIE
 ILKSLQHDNIVKYKGVCSAGRRL LIME
 ILKSLQHDNIVKYKGVCSAGRRLKLIME
 910 920 930
 901 ILKSLQHDNIVKYKGVCSAGRRL LIME
 901 ILKSLQHDNIVKYKGVCSAGRRLKLIME
 YLPYGS LR DY LQKHKERIDH KLLQYTSQI
 YLPYGS LR DY LQKHKERIDH KLLQYTSQI
 940 950 960
 931 YLPYGS LR DY LQKHKERIDH KLLQYTSQI
 931 YLPYGS LR DY LQKHKERIDH KLLQYTSQI
 CKGMEYLGTKRYIHRDLATRNILVENENRV
 CKGMEYLGTKRYIHRDLATRNILVENENRV
 970 980 990
 961 CKGMEYLGTKRYIHRDLATRNILVENENRV
 961 CKGMEYLGTKRYIHRDLATRNILVENENRV
 KIGDFGLTKVLPQDKEYYKVKEPGESPFIW
 KIGDFGLTKVLPQDKEYYKVKEPGESPFIW
 1000 1010 1020
 991 KIGDFGLTKVLPQDKEYYKVKEPGESPFIW
 991 KIGDFGLTKVLPQDKEYYKVKEPGESPFIW

FIGURE 2E

Y A P . S L T E S K F S V A S D V W S F G V V L Y E L F T Y
 Y A P E S L T E S K F S V A S D V W S F G V V L Y E L F T Y
 1030 1040 1050
 1021 **Y A P Q S L T E S K F S V A S D V W S F G V V L Y E L F T Y**
 1021 **Y A P E S L T E S K F S V A S D V W S F G V V L Y E L F T Y**
 I E K S K S P P . E F M R M I G N D K Q G Q M I V F H L I E
 I E K S K S P P A E F M R M I G N D K Q G Q M I V F H L I E
 1060 1070 1080
 1051 **I E K S K S P P V E F M R M I G N D K Q G Q M I V F H L I E**
 1051 **I E K S K S P P A E F M R M I G N D K Q G Q M I V F H L I E**
 L L K . N G R L P R P . G C P D E I Y . I M T E C W N N N V
 L L K S N G R L P R P D G C P D E I Y V I M T E C W N N N V
 1090 1100 1110
 1081 **L L K S N G R L P R P E G C P D E I Y V I M T E C W N N N V**
 1081 **L L K N N G R L P R P D G C P D E I Y M I M T E C W N N N V**
 . Q R P S F R D L I
 S Q R P S F R D L A L R V G Q I K D G T A G
 1120 1130
 1111 **S Q R P S F R D L S F - - G W I K C G T V .**
 1111 **N O R P S F R D L A L R V D Q I R D N M A G**

FIGURE 2F